

Page 2

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

RESULT 6	
DN33797	DN33797 standard; protein; 447 AA.
D	ADN23797
X	X
C	ADN33797;
X	X
T	02-DEC-2004 (first entry)
X	X
E	Bacterial polypeptide #6450.
X	X
W	Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
W	pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
W	W

X

Bacteria.

11S2003233675-A1

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18-DEC-2003.

X

20-FEB-2003; 200308-00369493.

21-FEB-2002: 2002US-0360039P.

— 1 —

A (CAOY/) CAO Y.

HINKLE

J. C. SLATER 5

GOLDMAN B. S.
GOLD/

I Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

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MEI/1
MEI/2
MEI/3
MEI/4
MEI/5
MEI/6

comprising a promoter positioned to provide

for expression of a polynucleotide encoding a polypeptide from a

microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 6450; 112pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a

XX	SQ	Sequence 447 AA;
XX	Qy	Query Match 51.0%; Score 50; DB 8; Length 447; Best Local Similarity 77.8%; Pred. No. 26; Matches 7; Conservative 2; Mismatches 0; Gaps 0;
XX	Db	Qy 1 CFFRGQQPN 9 Db 154 CFYRGQPYN 162
XX	AC	ADN23700 standard; protein; 511 AA.
XX	AC	ADN23700;
XX	DT	02-DEC-2004 (first entry)
XX	DE	Bacterial polypeptide #6353.
XX	KW	Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; Plant Growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; photosynthesis; lignin; galactomannan; bacterial phosphopeptide.
XX	KW	

XX OS Bacteria.
 XX US2003233675-A1.
 XX PD 18-DEC-2003.
 XX PF 20-FEB-2003; 2003US-00369493.
 XX PR 21-FEB-2002; 2002US-0360039P.
 XX PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX DR WPI; 2004-061375/06.
 XX PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a

XX Claim 1; SEQ ID NO 6353; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 511 AA;

Query Match 51.0%; Score 50; DB 8; Length 511;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CFFRGFFN 9
Db 204 CPyRGFVN 212

XX Sequence 136 AA;

Query Match 46.9%; Score 46; DB 6; Length 136;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FRGGFFENHPRYC 15
Db 106 FRGGTGTGHRPLC 118

XX RESULT 9

AAE09606
ID AAE09606 standard; protein; 166 AA.

XX AAE09606;

AC DT 19-NOV-2001 (first entry)

XX DB Human gene 14 encoded novel protein HMEC68, SEQ ID NO:42.

XX KW Human; cytostatic; gene therapy; inflammatory disorder; neural disorder; Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;

XX KW autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia;

XX KW reproductive disorder; Crohn's disease; pulmonary disorder; cancer;

XX KW myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour;

XX KW haematopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis;

XX KW drug screening; endocrine disorder; leukaemia.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 157
/label= Unknown
/note= "Encoded by MA"

XX PR XX WO200153311-A2.

XX PD 02-AUG-2001.

XX PP 17-JAN-2001; 2001WO-US001315.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-01886350P.

XX PR 16-MAR-2000; 2000US-019874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-020515P.

XX PR 07-JUN-2000; 2000US-0219467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-021647P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*
CC infection, this may be in the form of a vaccine or gene therapy. Sequences
CC given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention
XX SQ Sequence 136 AA;

Query Match 46.9%; Score 46; DB 6; Length 136;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 FRGGFFENHPRYC 15

Db 106 FRGGTGTGHRPLC 118

XX RESULT 9

AAE09606

ID AAE09606 standard; protein; 166 AA.

XX AAE09606;

AC DT 19-NOV-2001 (first entry)

XX DB Human gene 14 encoded novel protein HMEC68, SEQ ID NO:42.

XX KW Human; cytostatic; gene therapy; inflammatory disorder; neural disorder; Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia; reproductive disorder; Crohn's disease; pulmonary disorder; cancer; myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour; haematopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis; drug screening; endocrine disorder; leukaemia.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 157
/label= Unknown
/note= "Encoded by MA"

XX PR XX WO200153311-A2.

XX PD 02-AUG-2001.

XX PP 17-JAN-2001; 2001WO-US001315.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-01886350P.

XX PR 16-MAR-2000; 2000US-019874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-020515P.

XX PR 07-JUN-2000; 2000US-0219467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-021647P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0220964P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX WPI; 2003-058115/05.

XX N-PSDB; AB240759.

XX New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.

XX Disclosure; Page 634; 815pp; English.

PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0222267P.
 PR 14-AUG-2000; 2000US-0225168P.
 PR 14-AUG-2000; 2000US-0222270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225157P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-02252559P.
 PR 18-AUG-2000; 2000US-0226779P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 01-SEP-2000; 2000US-0226894P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0222287P.
 PR 01-SEP-2000; 2000US-0223343P.
 PR 01-SEP-2000; 2000US-0223344P.
 PR 05-SEP-2000; 2000US-0223345P.
 PR 05-SEP-2000; 2000US-0223509P.
 PR 05-SEP-2000; 2000US-0223513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0230808P.
 PR 08-SEP-2000; 2000US-0231081P.
 PR 12-SEP-2000; 2000US-0231319P.
 PR 14-SEP-2000; 2000US-0231244P.
 PR 14-SEP-2000; 2000US-02313397P.
 PR 14-SEP-2000; 2000US-02313398P.
 PR 14-SEP-2000; 2000US-02313399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0231065P.
 PR 21-SEP-2000; 2000US-0231232P.
 PR 25-SEP-2000; 2000US-0231274P.
 PR 25-SEP-2000; 2000US-0231997P.
 PR 26-SEP-2000; 2000US-0234998P.
 PR 27-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0235935P.
 PR 29-SEP-2000; 2000US-0236272P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 02-OCT-2000; 2000US-0236369P.
 PR 02-OCT-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 13-OCT-2000; 2000US-0239337P.
 PR 20-OCT-2000; 2000US-024060P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241788P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 08-NOV-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246747P.
 PR 08-NOV-2000; 2000US-0246778P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-OBC-2000; 2000US-0250160P.
 PR 01-OBC-2000; 2000US-0250391P.
 PR 05-OBC-2000; 2000US-0250300P.
 PR 05-OBC-2000; 2000US-0251988P.
 PR 05-OBC-2000; 2000US-0256199P.
 PR 06-OBC-2000; 2000US-025479P.
 PR 08-OBC-2000; 2000US-0251856P.
 PR 08-OBC-2000; 2000US-0251868P.
 PR 08-OBC-2000; 2000US-0251869P.
 PR 08-OBC-2000; 2000US-0251989P.
 PR 11-OBC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Claim 11; SEQ ID NO 42; 464P; English.

PI Rossen CA, Barash SC, Ruben SM, XX
 XX
 DR WPI: 2001-502629/55.
 DR N-PSDB; AAD16540.

XX PT New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing inflammatory, neural, immune system, muscular, reproductive, pulmonary, cardiovascular or proliferative disorders, or cancer.

XX PT New polynucleotides and polypeptides, useful for diagnosing, treating, preventing and/or prognosing inflammatory disorders (bursitis or tendonitis); neural disorders (e.g. Parkinson's disease, Alzheimer's disease); immune system disorders; AIDS; autoimmune diseases (e.g., rheumatoid arthritis); muscular disorders; reproductive disorders; gastrointestinal disorders (malabsorption syndrome, Crohn's disease); pulmonary disorders; cardiovascular disorders (myocardial infarction, ischaemia, arrhythmias); renal disorders (glomerulonephritis, nephrotic syndrome); cancerous disease and conditions (breast cancer, hyperproliferative disorders (leukaemia, hyperplasia); tumours; foetal and developmental abnormalities; haematopoietic disorders; respiratory disorders (rhinitis, asthma); angiogenic disorders; diabetes; endocrine disorders; pregnancy-related disorders and infections. The novel protein DNA is useful in gene therapy and drug screening. The proteins can also be used

CC AAD16527-AAD16544 represent cDNAs corresponding to novel human protein genes, and AAB0959-AAB19610 represent the proteins they encode. AAD16545-
 CC -AAD16572 represent novel human protein genes. The novel proteins and their
 CC DNAs are useful for diagnosing, treating, preventing and/or prognosing
 CC inflammatory disorders (bursitis or tendonitis); neural disorders (e.g.
 CC Parkinson's disease, Alzheimer's disease); immune system disorders; AIDS;
 CC autoimmune diseases (e.g., rheumatoid arthritis); muscular disorders;
 CC reproductive disorders; gastrointestinal disorders (malabsorption
 CC syndrome, Crohn's disease); pulmonary disorders; cardiovascular disorders
 CC (myocardial infarction, ischaemia, arrhythmias); renal disorders
 CC (glomerulonephritis, nephrotic syndrome); cancerous disease and
 CC conditions (breast cancer, hyperproliferative disorders (leukaemia,
 CC hyperplasia); tumours; foetal and developmental abnormalities;
 CC haematopoietic disorders; respiratory disorders (rhinitis, asthma);
 CC angiogenic disorders; diabetes; endocrine disorders;
 CC pregnancy-related disorders and infections. The novel protein DNA is
 CC useful in gene therapy and drug screening. The proteins can also be used

CC to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, to support cell culture of primary tissues, to regenerate tissues, to

CC

Query Match 46.9%; Score 46; DB 4; Length 166;

Best Local Similarity 40.0%; Pred. No. 41;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFFRGCGFFINPRYC 15

Db 114 CYYGDGFFGBNNEFC 128

RESULT 10

ABG78978 ABG78978 standard; protein; 166 AA.

XX

ABG78978;

AC

XX

DT 15-NOV-2002 (first entry)

XX

DE Human apoptosis related protein fromcDNA clone HMMEC08.

KW Human; apoptosis related protein; immunodeficiency;

KW B cell immunodeficiency; severe combined immunodeficiency; gene therapy;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; asthma;

KW diabetes mellitus; allergy; inflammatory condition; thrombosis;

KW graft-versus-host disease; blood-related disorder; atherosclerosis;

KW hyperproliferative disorder; cardiovascular disorder; arrhythmia;

KW acute glomerulonephritis; cardiovascular disorder; respiratory disorder;

KW Goodpasture's syndrome; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; endocrine disorder; Addison's disease;

KW reproductive system disorder; endometriosis; infection; Crohn's disease;

KW gastrointestinal disorder.

XX

OS Homo sapiens.

XX

PN US2002086811-A1.

XX

PD 04-JUL-2002.

XX

PF 17-JAN-2001; 2001US-00764861.

XX

PR 31-JAN-2000; 2000US-01790655P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217495P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0222964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0222287P.

PR 01-SEP-2000; 2000US-0223343P.

PR 01-SEP-2000; 2000US-0223344P.

PR 01-SEP-2000; 2000US-0223345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 08-SEP-2000; 2000US-0231413P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234199P.

PR 27-SEP-2000; 2000US-0235834P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-023935P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.

PR 17-NOV-2000; 2000US-0249299P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

XX

PA (ROSE/) ROSEN C A.

PA (ROBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX

PI Rosen CA, Ruben SM, Barash SC;

XX

DR WPI: 2002-642253/69.

DR N-PSDB; ABS6130.

XX

PT Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.

XX

PS Claim 11; Page 197; 258pp; English.

XX

CC The invention relates to 18 apoptosis related proteins (or proteins 90% similar to them) and their encoding nucleic acids (including fragments, allelic variants and nucleic acids hybridizing to them). Also included are vectors, host cells, antibodies, method of detecting the activity of the proteins, and the genes for the proteins. The nucleic acids, proteins and antibodies are useful for diagnosing and/or treating, prognosis or preventing immunodeficiencies (e.g. B cell immunodeficiencies, severe combined immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple sclerosis, diabetes mellitus), allergic reactions and conditions (e.g. asthma), inflammatory conditions, graft-versus-host disease, blood-related disorders (thrombosis, atherosclerosis), hyperproliferative disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease), endocrine disorders (e.g. Addison's disease), reproductive system disorders (e.g. endometriosis), infectious diseases (e.g. viral, bacterial or fungal infections), and infectious gastrointestinal disorders (e.g. Crohn's disease). The protein is also useful for identifying a binding partner to the polypeptide. The protein is also useful for stimulating keratinocyte growth, to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coactors or other nutritional components. The present sequence represents a human apoprosis related protein of the invention

XX

SQ Sequence 166 AA;

Query Match 46.9%; Score 46; DB 5; Length 166;

Best Local Similarity 40.0%; Pred. No. 41;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFFRGCGFFINPRYC 15

Db 114 CYYGDGFFGBNNEFC 128

RESULT 11

ID AAE39806 Standard; protein; 166 AA.

XX AAE39805;

XX DT 18-DEC-2003 (first entry)

XX DE Human gene 14-encoded secreted protein HMMEC68, SEQ ID NO:42.

XX KW Bruton's disease; immunodeficiency; Chediak-Higashi syndrome; Hashimoto's thyroiditis; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis; Goodpasture's syndrome; Parkinson's disease; multiple sclerosis; haemolytic anaemia; Addison's disease; rhinitis; Sjogren's syndrome; cardio-vascular disorder; Alzheimer's disease; neurodegenerative disorder; atherosclerosis; inflammation; allergy; adrenocortical; cholecytosis; keratitis; retinitis; CNS disorder; myocarditis; polymyelitis; gene therapy; asthma; ischaemia; stroke.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 157 /note= "Encoded by MA"

XX US2003092615-A1.

PD 15-MAY-2003.

XX PP 05-APR-2002; 2002US-00115928.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180668P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0188714P.

PR 17-MAR-2000; 2000US-0190976P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-020467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-AUG-2000; 2000US-0217496P.

PR 26-JUL-2000; 2000US-02218290P.

PR 14-AUG-2000; 2000US-0222114P.

PR 14-AUG-2000; 2000US-0222214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225767P.

PR 14-AUG-2000; 2000US-022518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225113P.

PR 14-AUG-2000; 2000US-0225147P.

PR 23-AUG-2000; 2000US-0225157P.

PR 14-AUG-2000; 2000US-0225265P.

PR 14-AUG-2000; 2000US-0225759P.

PR 22-AUG-2000; 2000US-0225268P.

PR 22-AUG-2000; 2000US-0225681P.

PR 22-AUG-2000; 2000US-022668P.

PR 23-AUG-2000; 2000US-0227182P.

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PR 01-SEP-2000; 2000US-0223343P.

PR 01-SEP-2000; 2000US-0223344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 12-SEP-2000; 2000US-0232081P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-02334223P.

PR 21-SEP-2000; 2000US-02334274P.

PR 25-SEP-2000; 2000US-02334998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-02336327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

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PR 13-OCT-2000; 2000US-023935P.

PR 13-OCT-2000; 2000US-023937P.

PR 20-OCT-2000; 2000US-024060P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 08-NOV-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0241827P.

PR 08-NOV-2000; 2000US-0241867P.

PR 08-NOV-2000; 2000US-024174P.

PR 08-NOV-2000; 2000US-0246475P.

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PR 08-NOV-2000; 2000US-0246526P.

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PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P. DE Novel human secreted protein #1478.
 PR 17-NOV-2000; 2000US-024916P. XX
 PR 17-NOV-2000; 2000US-0249217P. KW Human; vaccination; gene therapy; nutritional supplement;
 PR 17-NOV-2000; 2000US-0249218P. KW stem cell proliferation; haematoepoiesis; nerve tissue regeneration;
 PR 17-NOV-2000; 2000US-024944P. KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 PR 17-NOV-2000; 2000US-0249264P. XX
 PR 17-NOV-2000; 2000US-0249297P. OS Homo sapiens.
 PR 17-NOV-2000; 2000US-0249299P. XX
 PR 17-NOV-2000; 2000US-0249300P. PN WO200179449-A2.
 PR 01-DEC-2000; 2000US-0249300P. XX
 PR 01-DEC-2000; 2000US-0250160P. PD 25-OCT-2001.
 PR 05-DEC-2000; 2000US-0250391P. XX
 PR 05-DEC-2000; 2000US-025130P. PF 16-APR-2001; 2001WO-US008655.
 PR 05-DEC-2000; 2000US-025130P. XX
 PR 05-DEC-2000; 2000US-0256719P. PR 18-APR-2000; 2000US-00552929.
 PR 06-DEC-2000; 2000US-0251479P. PR 26-JAN-2001; 2001US-00770160.
 PR 08-DEC-2000; 2000US-0251856P. XX
 PR 08-DEC-2000; 2000US-0251868P. PA (HYSE-) HYSEQ INC.
 PR 08-DEC-2000; 2000US-0251869P. XX
 PR 08-DEC-2000; 2000US-0251988P. PI Tang YT, Liu C, Drmanac RT;
 PR 08-DEC-2000; 2000US-0256719P. XX
 PR 11-DEC-2000; 2000US-0251990P. DR WPI; 2001-611725/70.
 PR 05-JAN-2001; 2001US-0254097P. XX
 PR 17-JAN-2001; 2001US-00764861. PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy. XX
 PA (HUMA-) HUMAN GENOME SCI INC. PS Claim 20, Page 386; 76pp; English.
 XX
 PI Rosen CA, Ruben SM, Barash SC; PS
 XX
 DR WPI: 2003-765488/72. XX
 N-PSDB; AAD60439. XX
 PT New isolated nucleic acids and their encoded polypeptides potentially
 PT useful for diagnosing and treating disease. XX
 PS Claim 1; Page 195-196; OPP; English.
 XX
 AAD60426-AAD60443 represent cDNAs corresponding to 17 human secreted
 CC protein genes and AAE39793-AAE39810 represent the proteins they encode.
 CC AAB0444-AAD60471 represent human genomic DNAs. The invention is useful
 CC for preventing, treating or ameliorating immunodeficiencies such as
 CC Bruton's disease, Wiskott-Aldrich syndrome and Chediak-Higashi syndrome,
 CC autoimmune disorders such as Hashimoto's thyroiditis, systemic lupus
 CC erythematosus, rheumatoid arthritis, myasthenia gravis, Goodpasture's
 CC syndrome, multiple sclerosis, haemolytic anaemia, Addison's disease and
 CC Sjogren's syndrome, allergic reactions such as asthma, rhinitis and
 CC eczema. The invention is also useful in the treatment of tissue-specific
 CC inflammatory disorders such as adrenaititis, cholecytitis, keratitis,
 CC retinitis and polyneuritis, CNS disorders such as stroke and ischaemia,
 CC cardio-vascular disorders such as atherosclerosis and myocarditis and
 CC neurodegenerative disorders such as Parkinson's disease and Alzheimer's
 CC disease. The invention is also useful in gene therapy. The present
 CC sequence represents a human secreted protein of the invention
 XX Sequence 166 AA.
 SQ Query Match 46.9%; Score 46; DB 4; Length 406;
 Best Local Similarity 40.0%; Pred. No. 97; XX
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0; Gaps 0;
 AC AAB61307; XX
 AC AAB61307; AC
 AC AAB61307; XX
 AC AAB61307; DT 30-MAR-2001 (first entry)
 AC AAB61307; XX
 AC AAB61307; DE Human transcriptional regulator protein #7.
 AC AAB61307; KW Homo sapiens.
 AC AAB61307; OS XX
 AC AAB61307; PN WO200078954-A2.

CC nucleic acid or vector in the cells. The presence of the proteinaceous
CC substance is detected by immuno-staining the cells with the antibody.
CC They may also be used to identify a putative cancer-inducing agent (e.g.
CC a genome or functional fragment) by contacting a cell sample with a
CC candidate agent and detecting the presence of cancer cells (or cancer-
CC prone cells). They may also be used to identify a putative effector of the
CC activity of protein, by binding it with a candidate effector and
CC determining it's binding
XX

SQ Sequence 876 AA;

Query Match 46.9%; Score 46; DB 4; Length 876;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFPFGGFENHNPYC 15
Db 296 CYGDGFGENNEFC 310

Search completed: October 4, 2005, 22:12:12
Job time : 168 secs

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OM protein - protein search, using sw model

Run on: October 4, 2005, 22:01:05 ; Search time 39 Seconds
 37.006 Million cell updates/sec

Title: US-10-633-423-2

Perfect score: 98

Sequence: 1 CFPGGFFNNPRYC 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Database : PIR_79;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*
 4: pir4;*

Listing First 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.5	54.6	453	2 T24127	probable chitinase
2	50	51.0	272	2 T20139	hypothetical prote
3	50	51.0	447	2 T19078	hypothetical prote
4	50	51.0	511	2 T31899	hypothetical prote
5	45	45.9	433	2 H84055	UDP-N-acetylglucosamine phospho
6	44	44.9	277	2 AD0809	xanthosine phospho
7	44	44.9	365	2 JC7527	nucleic acid viral
8	44	44.9	708	1 A43717	alpha-D-galactosidase
9	44	44.9	1291	2 T13389	hypothetical prote
10	43	43.9	134	2 S46106	probable membrane
11	43	43.9	373	2 F86382	hypothetical prote
12	43	43.9	660	2 AH23458	hypothetical prote
13	42	42.9	124	2 C965559	F5F19.3 (imported)
14	42	42.9	439	2 H82875	oligopeptide trans
15	42	42.9	473	2 A56175	adhesive plaque pr
16	42	42.9	1477	2 T18534	protein-tirosine k
17	41	41.8	237	2 T34473	hypothetical prote
18	41	41.8	373	1 WMBET6	UL16 protein - hum
19	41	41.8	501	2 A90595	carboxylic acid synth
20	41	41.8	537	2 H84642	hypothetical prote
21	41	41.8	658	2 T50080	probable DNA repair
22	41	41.8	826	2 G97073	uncharacterized pr
23	40	40.8	143	2 E72349	conserved hypothet
24	40	40.8	273	2 AH2432	hypothetical prote
25	40	40.8	412	2 S62538	hypothetical coile
26	40	40.8	442	2 AB0964	regulatory prote
27	40	40.8	442	2 C41853	hexose phosphate
28	40	40.8	462	2 T05995	hypothetical prote
29	40	40.8	638	1 KQHUP	plasma kallikrein

probable protein k
 lysine decarboxyla
 lysine decarboxyla
 lysine decarboxyla
 hypothetical prote
 dual specificity p
 hypothetical prote
 probable disease r
 hypothetical prote
 hypothetical prote
 hypothetical prote
 hypothetical prote
 hypothetical prote
 tmRNA-binding prot

ALIGNMENTS

RESULT 1

T24127

Probable chitinase (EC 3.2.1.14) precursor R10D12.15 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24127; T25316; T25318

R;Percy, C.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19842

A;Accession: T24127

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-453 < WIL>

A;Cross-references: UNIPROT: P92013; EMBL: 281109; PIDN: CAB03255.1; GSPDB: GN00023; CESP: R10D12.15

R;Percy, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20014

A;Accession: T25316

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-453 < WI2>

A;Cross-references: EMBL: Z82054; PIDN: CAB04840.1; GSPDB: GN00023; CESP: T26F2.1

A;Accession: T25318

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-453 < WI3>

A;Cross-references: EMBL: Z82054; PIDN: CAB04842.1; GSPDB: GN00023; CESP: R10D12.15

A;Accession: T26F2

A;Experimental source: clone T26F2

C;Genetics:

A;Gene: CESP: R10D12.15; CESP: T26F2.1

A;Map position: 5

A;Introns: 23/1: 118/3: 150/2: 237/3: 3 69/1

C;Keywords: glycosidase, hydrolase

Query Match 54.6%; Score 53.5; DB 2; Length 453;

Best Local Similarity 28.6%; Pred. No. 0.57%; Matches 12; Conservative 3; Mismatches 0; Indels 27; Gaps 2;

QY 1 CFPFGFFN-----HNP-----RYC 15

Db 160 CFYRGFGYNWFGGPPSSNLFNLPETPGHSPTDGNSCTSAGRYC 201

RESULT 2

T20139

Hypothetical protein C51E3.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20139

R;Wilkinson, J.

Submitted to the EMBL Data Library, August 1996

A; Reference number: Z19227

A; Status: Preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-272 <WIL>

A; Cross-references: UNIPROT:Q01981; EMBL:Z78410; PIDN:CAB01643.1; GSPDB:GN00023; CESP:CESP

A; Experimental source: clone C51E3

C; Genetics:

A; Gene: CESP:CG1E3.8

A; Map position: 5

A; Introns: 3B/3; 117/3

Query Match

Score 51.0%; DB 2; Length 272;

Best Local Similarity 77.8%; Pred. No. 1.3;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFRGFFN 9

Db 157 CFYRGFFYN 165

RESULT 3

T19078 hypothetical protein C08B6.4 - *Caenorhabditis elegans*C; Species: *Caenorhabditis elegans*

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C; Accession: T19078

R; Wilkinson, J.

Submitted to the EMBL Data Library, May 1996

A; Reference number: Z19070

A; Status: Preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-447 <WIL>

A; Cross-references: UNIPROT:Q17816; EMBL:Z72502; PIDN:CAA96587.1; GSPDB:GN00023; CESP:CESP

A; Experimental source: clone C08B6

C; Genetics:

A; Gene: CESP:CG08B6.4

A; Map position: 5

A; Introns: 17/1; 112/3; 144/2; 363/1

Query Match

Score 51.0%; DB 2; Length 447;

Best Local Similarity 77.8%; Pred. No. 2.1;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFRGFFN 9

Db 154 CFYRGFFYN 162

RESULT 4

T31999 hypothetical protein T05H4.7 - *Caenorhabditis elegans*C; Species: *Caenorhabditis elegans*

C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C; Accession: T31899

R; Blanchard, M.

Submitted to the EMBL Data Library, July 1997

A; Description: The sequence of *C. elegans* cosmid T05H4.

A; Reference number: Z21097

A; Status: Preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-511 <BLA>

A; Cross-references: UNIPROT:Q16452; PIDN:AF016452; GSPDB:GN00023; CESP:

A; Experimental source: strain Bristol N2; clone T05H4

C; Genetics:

A; Gene: CESP:T05H4.7

A; Map position: 5

A; Introns: 76/1; 192/2; 229/1; 414/1

Query Match

Score 51.0%; DB 2; Length 511;

Best Local Similarity 77.8%; Pred. No. 2.4; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFRGFFN 9

Db 204 CFYRGFFYN 212

RESULT 5

H84055 UDP-N-acetylglucosamine ligase murC [imported] - *Bacillus halodurans* (strain C-125)C; Species: *Bacillus halodurans*

C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C; Accession: H84055

R; Nakano, H.; Nakano, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, A.

Nucleic Acids Res. 28, 4317-4331, 2000

A; Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and .

A; Reference number: A83650; MUID:20512582; PMID:11058132

A; Accession: H84055

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-433 <STO>

A; Cross-references: UNIPROT:Q9K7N1; GB:AP001518; GB:BA000004; PIDN:BA000004; PIDN:BA000004

A; Experimental source: strain C-125

C; Genetics:

A; Gene: murC

C; Superfamily: UDP-N-acetylglucosamine ligase

Query Match

Score 45.9%; DB 2; Length 433;

Best Local Similarity 44.7%; Pred. No. 13;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFFRGFFNHNPNYC 15

Db 152 CEYRRHFLNRPDYC 166

RESULT 6

AD0809 xanthine phosphotriphosphorylase (EC 2.4.2.-) [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi*C; Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*A; Note: This species has also been called *Salmonella typhi*

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C; Accession: AD0809

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moulton, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar

A; Reference number: AB0502; MUID:21534947; PMID:11677608

A; Accession: AD0809

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-277 <PAR>

A; Cross-references: GB:AL513382; PIDN:CAD07654.1; PIDN:G000176

C; Genetics:

A; Gene: STY2658

C; Superfamily: purine-nucleoside phosphorylase

C; Keywords: glycosyltransferase; pentosyltransferase

Query Match

Score 44%; DB 2; Length 277;

Best Local Similarity 75.0%; Pred. No. 12;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 FNHNPYC 15

Db 6 FSHNPBYC 13

RESULT 7

JC7327 nuclear retroviral polymerase-like protein - rat

C;Species: *Rattus norvegicus* (Norway rat)
 C;Accession: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C;Accession: JC7527
 R;Graham, K.M.; Ko, C.; Park, K.; Sarge, K.; Park-Sarge, O.K.
 Biochem. Commun. 278, 48-7, 2000
 A;Title: Expression of an intracisternal A-particle-like element in rat ovary
 A;Reference number: JC7527; MUID:20525406; PMID:11071854
 A;Content: ovary, granulosa cells
 A;Accession: JC7527
 A;Molecule type: mRNA
 A;Residues: 1-365 <GRA>
 A;Cross-references: GB:AB964260
 C;Comment: This protein is involved in cell proliferation, differentiation, folliculogenesis
 C;Genetics:
 A;Gene: laptene
 C;Keywords: ovary; transformation
 Query Match Score 44; DB 2; Length 365;
 Best Local Similarity 53.8%; Pred. No. 16;
 Matches 2; Indels 0; Gaps 0;
 Qy 1 CFFRGFFENINPR 13
 Db 276 CYFDGFEDNHYPK 288

RESULT 8

A43717
 alpha-galactosidase (EC 3.2.1.22), raffinose-specific - *Escherichia coli* plasmid D1021
 C;Species: *Escherichia coli*
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A43717; B35160
 R;Asianidis, C.; Schmidt, K.; Schmitt, R.
 J. Bacteriol. 171, 6753-6763, 1989
 A;Title: Nucleotide sequences and operon structure of plasmid-borne genes mediating uptake
 A;Reference number: A43717; MUID:90078124; PMID:2556373
 A;Accession: A43717
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-708 <ASL>
 A;Cross-references: UNIPROT:PI16551; GB:M27273; NID:9147504; PID:g147505
 R;Asianidis, C.; Schmidt, R.
 J. Bacteriol. 172, 2178-2180, 1990
 A;Title: Regulatory elements of the raffinose operon: nucleotide sequences of operator and promoter regions
 A;Reference number: A35160; MUID:90202743; PMID:180920
 A;Accession: B35160
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <AS2>
 A;Cross-references: GB:M29849; NID:g147508; PID:AAA24501.1; PID:g5511828
 C;Genetics:
 A;Gene: rafa
 A;Genome: plasmid
 C;Complex: homotetramer
 C;Function:
 C;Description: catalyzes the hydrolysis of raffinose to galactose and sucrose
 C;Keywords: glycoprotein; glycosidase; hydrolase
 Query Match Score 44; DB 1; Length 708;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 2; Indels 0; Gaps 0;
 Qy 3 FRGGFFNHNPY 14
 Db 299 WEGIYFNHNPDY 310

RESULT 9

T13389
 hypothetical protein 115G2.10 - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T13389
 R;Salle, C.; Valenti, P.; Darlamitou, A.; Henderson, N.; Campbell, L.; Glover, D.
 Submitted to the EMBL Data Library, May 1999
 A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A;Reference number: Z17665
 A;Accession: T13389
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1291 <CAT>
 A;Cross-references: UNIPROT:Q77261; EMBL:AL031581; NID:e1320978; PID:e1426292; PIDN:CAA2
 A;Cross-references:
 A;Cross-references: FlyBase:FBgn0020381.
 A;Map position: X
 A;Map position: 1225/1
 A;Note: EG:11;C2.10

Query Match Score 44%; DB 2; Length 1291;
 Best Local Similarity 46.7%; Pred. No. 57;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CFFRGFFFNINPRYC 15
 Db 363 CYYGEDFFGDSNRYC 377

RESULT 10

S46106
 probable membrane protein YBR230C - yeast (*Saccharomyces cerevisiae*)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C;Accession: S46106
 R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;
 submitted to the Protein Sequence Database, August 1994
 A;Reference number: S45782
 A;Accession: S46106
 A;Molecule type: DNA
 A;Residues: 1-134 <DUB>
 A;Cross-references: UNIPROT:P38325; EMBL:Z36099; NID:9536627; PID:9536628; GSPPDB:GN00002
 C;Genetics:
 A;Gene: MIPS:YBR230C
 A;Cross-references: SGD:S0000434
 A;Map position: 2R
 A;Introns: 4/2
 C;Superfamily: *Saccharomyces* probable membrane protein YBR230C
 C;Keywords: transmembrane protein
 F;70-88/Domain: transmembrane #status predicted <TM1>
 F;107-123/Domain: transmembrane #status predicted <TM2>

Query Match Score 43%; DB 2; Length 134;
 Best Local Similarity 42.9%; Pred. No. 8.5;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFFRGFFFNINPRY 14
 Db 84 CYLNGYANHARF 97

RESULT 11

F86382
 hypothetical protein F4P7.14 - *Arabidopsis thaliana* (mouse-ear cress)
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C;Accession: F86382
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Hansen, N.E.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Accession: A86141; MUID:21016719; PMID:11130712

A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-373 <STO>
 A;Cross-references: GB:AE005172; NID:911067280; PIDN:AAG28808.1; GSPDB:GN00141

A;Genetics:
 A;Map position: 1

Query Match 43.9%; Score 43; DB 2; Length 373;
 Best Local Similarity 61.5%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Query 1 CFFRGFFENPR 13
 Db 121 CFFNGGESSRLNPR 133

RESULT 12

AH2348 hypothetical protein a114343 [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AH2348
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A;Accession: AH2348
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-660 <KUR>
 A;Cross-references: UNIPROT:Q8YP57; GB:BA000019; PIDN:BAB76042.1; PID:gi171333479; GSPDB:GN00141

A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: a114343

Query Match 43.9%; Score 43; DB 2; Length 660;
 Best Local Similarity 70.0%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query 5 GGFFENPRY 14
 Db 387 GGYFNRRNY 396

RESULT 13

C96559 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: C96559
 R;Theology, A.; Bicker, J.R.; Palm, C.J.; Federspiel, N.A.; Kau, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Andersen, N.F.; Hughes, B.; Huijzer, L.
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Accession number: A86141; MUID:21016719; PMID:11130712

A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <STO>
 A;Cross-references: UNIPROT:Q9ZU26; GB:AE005173; NID:g4220444; PIDN:AAD12671.1; GSPDB:GN00141

C;Genetics:

A;Gene: P5F19.3
 A;Map position: 1

Query Match 42.9%; Score 42; DB 2; Length 124;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Query 1 CFFRGFFN 9
 Db 86 CMFRGWN 94

RESULT 14

H82875 oligopeptide transport system permease protein U559 [imported] - *Ureaplasma urealyticum*
 C;Species: *Ureaplasma urealyticum*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000

A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a min

A;Reference number: AB2870

A;Accession: H82875
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-439 <GLA>
 A;Cross-references: GB:AB002154; GB:AT222894; NID:96899557; PIDN:AAF30972.1; GSPDB:GN0011

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: CppF; U559

A;Genetic code: SGCG3

Query Match 42.9%; Score 42; DB 2; Length 439;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query 7 FFFNHPRYC 15
 Db 10 FFFNHKRF 18

RESULT 15

A56175 adhesive plaque protein Mgfp2 Precursor - Mediterranean mussel
 C;Species: *Mytilus Galloprovincialis* (Mediterranean mussel)
 C;Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C;Accession: A56175
 R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
 J. Biol. Chem. 270, 6698-6704, 1995

A;Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth facto

A;Reference number: A56175; MUID:9520464; PMID:7896812

A;Accession: A56175

A;Molecule type: mRNA

A;Residues: 1-473 <INO>

A;Cross-references: UNIPROT:Q25464; GB:D43794; NID:9502767.1; PID:BA007852.1; PMID:di00843

C;Keywords: duplication

F;1-17/Domain: Signal sequence #Status predicted <SIG>

F;38-419/Domain: EGF homology <EGF>

F;429-460/Domain: EGF homology <EGF>

F;23,36,43,56,75,382,424,455,468,473/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #

Query Match 42.9%; Score 42; DB 2; Length 473;
 Best Local Similarity 30.4%; Pred. No. 44;
 Matches 7; Conservative 4; Mismatches 4; Indels 8; Gaps 1;

Query 1 CFFRGFFENHNN-----PRYC 15
 Db 69 CFCKGYYGYNCLRNACKENQ 91

Search completed: October 4, 2005, 22:17:47
 Job time : 41 secs

RESULT 4	Q17816	PRELIMINARY;	PRT;	447 AA.	RP	SEQUENCE FROM N.A.
ID	Q17816;				RC	STRAIN=Bristol N2;
AC	Q17816;	(TREMBrel. 01, Created)			RA	Wilkinson J. I.
DT	01-NOV-1996	(TREMBrel. 01, Last sequence update)			RL	Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DT	01-NOV-1996	(TREMBrel. 24, Last annotation update)			DR	EMBL; Z72502; CAH19081.1; -.
DT	01-JUN-2003	(TREMBrel. 24, Last annotation update)			DR	InterPro; IP000726; Glyco_hydro_19.
DT					DR	Pfam; PF00182; Glyco_hydro_19; 1.
DE	Hypothetical protein C08B6_4a;				DR	ProDom; PD354900; Glyco_hydro_19; 1.
GN	Name=C08B6_4a; ORFNames=C08B6_4;				KW	Hypothetical protein.
OS	Caenorhabditis elegans.				SQ	SEQUENCE 484 AA; 53734 MW; E1EDFSE8CFB8A46 CRC64;
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderaidae; Caenorhabditis.				Query Match	Score 50; DB 2; Length 484;
NCBI TaxID=6239;					Best Local Similarity	51.0%; Pred. No. 13;
RN	[1]				Matches	7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
RP	SEQUENCE FROM N.A.				Qy	1 CFPFGGFFN 9
RC	STRAIN=Bristol N2;				Db	191 CFYRGGFYN 199
MEDLINE=99069613; PubMed=9851916;						
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RL	Science 282:2012-2018 (1998).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	Wilkinson J. I.					
DT	Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.					
EMBL; Z72502; CAH19081.1; -.						
PIR; T19078; T19078.						
HSSP; P21951; 2BAA.						
DR	WormBase; WBGene0007425; C08B6_4.					
DR	WormPep; C08B6_4; CE05241.					
DR	GO:0004568; F:chitinase activity; IEA.					
DR	GO:0016998; P:cell wall catabolism; IEA.					
DR	GO:0006032; P:chitin catabolism; IEA.					
DR	GO:0009613; P:response to pest, pathogen or parasite; IEA.					
DR	InterPro; IPR00726; Glyco_hydro_19.					
DR	Pfam; PF00182; Glyco_hydro_19; 1.					
KW	Hypothetical protein.					
SEQUENCE	447 AA; 49503 MW;					
RN	6B4EC67A89B13D17 CRC64;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	Blanchard M. J.					
DT	Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	Waterson R. J.					
DT	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RG	WormBase Consortium;					
RL	Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL; AF016432; AAB66013.1; -.					
DR	PIR; T31899; T31899.					
DR	HSSP; P23951; 2BAA.					
DR	WormBase; WBGene00020270; T05H4_7.					
DR	WormPep; T05H4_7; CE13281.					
DR	GO; GO:004568; P:chitinase activity; IEA.					
DR	GO; GO:0016998; P:cell wall catabolism; IEA.					
DR	GO; GO:0006032; P:chitin catabolism; IEA.					
DR	GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
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RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology".					
RN	Science 282:2012-2018 (1998).					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Bristol N2;					
RA	none;					
RT	"Genome sequence of the					

Best Local Similarity 77.8%; Pred. No. 14; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	DR GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
Qy 1 CFFRGFFFN 9 Db 204 CFYRGFFYN 212	DR GO:0005975; P:carbohydrate metabolism; IEA.
	DR GO:0016938; P:cell wall catabolism; IEA.
	DR GO:0006032; P:chitin catabolism; IEA.
	DR GO:0009613; P:response to pest, pathogen or parasite; IEA.
	DR Pfam: PF00182; Glyco_hydro_19.
RESULT 7	KW Glycosidase; Hydrolase.
Q9XZ29 ID Q9XZ29 PRELIMINARY; PRT; 338 AA.	FT NON_TER 1 1 MW; C1E9BB91D2B65B1 CRC64;
AC Q9XZ29; 01-NOV-1999 (TREMBLrel. 12, Created) DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	SQ SEQUENCE 441 AA; 4941 MW; C1E9BB91D2B65B1 CRC64;
DE Bicoid protein (Fragment). GN Nameabccd; OS Megasabccd; OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Platypoda; Endopterygota; Diptera; Brachycera; Muscomorpha; NCBI_TaxID=88686; RN [1]	Query Match 48.0%; Score 47; DB 2; Length 441; Best Local Similarity 66.7%; Pred. No. 37; Gaps 0;
SEQUENCE FROM N.A. MEDLINE=19199462; PubMed=10097115; DOI=10.1073/pnas.96.7.3786; RX Sträuber M., Jaeger H., Schmidt-Ott U.; RA "The anterior determinant bicoid of <i>Drosophila</i> is a derived Hox class 3 gene.", RT "The anterior determinant bicoid of <i>Drosophila</i> is a derived Hox class 3 gene.", RL Proc. Natl. Acad. Sci. U.S.A. 96:3786-3789(1999). CC 1--SUBCELLULAR LOCATION: Nuclear (By similarity). EMBL: AU33024; CAB40892.1 -. HSSP: P33297; IIG7 DR GO:0005634; C: nucleolus; IEA. GO: GO:0003700; P: regulation of transcription, DNA-dependent; IEA. InterPro: IPR001355; P: regulation of transcription, DNA-dependent; IEA. PFam: PF00046; Homeobox; 1. PRTNS; PR00024; HOMEOBOX. DR SMART; SM00389; Hox; 1. InterPro: IPR009055; Homeobox. DNA-binding; Homeobox; Nucleotide protein. NON_TER 338 338 AA; 37818 MW; D5QD16E7096E7DE1 CRC64;	DR GO:0016798; P:hydrolase activity; IEA.
SEQUENCE 338 AA; 37818 MW; D5QD16E7096E7DE1 CRC64;	DR GO:0005975; P:carbohydrate metabolism; IEA.
Q962Y5 ID Q962Y5 PRELIMINARY; PRT; 441 AA.	DR GO:0016938; P:cell wall catabolism; IEA.
AC Q962Y5; 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DR GO:0006032; P:chitin catabolism; IEA.
DE Putative chitinase (EC 3.2.1.14) (Fragment). OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea) Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea. NCBI_TaxID=6233;	DR GO:0009613; P:response to pest, pathogen or parasite; IEA.
RN [1]	DR Pfam: PF00182; Glyco_hydro_19.
SEQUENCE FROM N.A. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. RN [1]	DR SMART; SM00050; FN3; 3.
Qy 1 CFFRGFFFN 11 Db 205 CFASGYFFN 215	DR SMART; SM00251; FU; 2.
	DR SMART; SM00219; TyrK; 1.
	DR PROSITE; PS50853; FN3; 2.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
RESULT 8	DR PRODOM; PD000001; Prot kinase; 1.
Q962Y5 ID Q962Y5 PRELIMINARY; PRT; 441 AA.	DR SMART; SM00050; FN3; 3.
AC Q962Y5; 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DR SMART; SM00251; FU; 2.
DE Putative chitinase (EC 3.2.1.14) (Fragment). OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea) Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea. NCBI_TaxID=6233;	DR SMART; SM00219; TyrK; 1.
RN [1]	DR PROSITE; PS50853; FN3; 2.
SEQUENCE FROM N.A. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. RN [1]	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
Qy 1 CFFRGFFFN 11 Db 205 CFASGYFFN 215	DR SMART; SM00050; FN3; 3.
	DR SMART; SM00251; FU; 2.
	DR SMART; SM00219; TyrK; 1.
	DR PROSITE; PS50853; FN3; 2.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

RA	Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T., Hori F., Imotani K., Ishii Y., Ichin M., Kagawa T., Kasukawa T., Kato J., Kawai J., Kojima Y., Kondo S., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Sasaki D., Saitoh H., Sakai C., Sakai T., Sakazume N., Sano H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A./GenBank/DBDB databases.	Submitted (APR-2002) to the EMBL/GenBank/DBDB databases.	GN	OrderredlocusName=TDE1739; Treponema denticola.
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Sasaki D., Saitoh H., Sakai C., Sakai T., Sakazume N., Sano H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A./GenBank/DBDB databases.	CC -1- SIMILARITY: Contains 1 SET domain.	OC	Bacteria; Spirochaetes; Spirochaetaceae; Treponema.
RA	Submitted (APR-2002) to the EMBL/GenBank/DBDB databases.	CC -1- SIMILARITY: Contains 1 SET domain.	NCBI_TaxID=158;	NCBI_TaxID=158;
RA	GO:0000780; C:condensed nuclear chromosome, pericentric r. . . ; IDA.	GO: GO:0016799; P:histone lyine N-methyltransferase activity . . . ; IDA.	RA	SEQUENCE FROM N.A.
RA	GO: GO:0016571; P:histone methylation; IDA.	IntePro: IPR001214; SET.	RA	STRAIN=TCC 35405 / DSM 14222;
RA	SMART: SM00317; SET; 1.	PROSITE: PS50280; SET; 1.	RA	PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA	PROSITE: PS50280; SET; 1.	PROSITE: PS50280; SET; 1.	RA	RA
RA	SEQUENCE 318 AA; MW: 36500 MW;	SEQUENCE 318 AA; MW: 69CD8984CC084CA6 CRC64;	RA	RA
RA	Query Match 46.9%; Score 46; DB 2; Length 318;	Query Match 46.9%; Score 46; DB 2; Length 318;	RA	RA
RA	Best Local Similarity 40.0%; Pred. No. 38;	Best Local Similarity 40.0%; Pred. No. 38;	RA	RA
RA	Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	RA	RA
Qy	1 CFFRGFFNNPRYC 15	1 CFFRGFFNNPRYC 15	RA	RA
Db	297 CYYGDSFFGENNEFC 311	297 CYYGDSFFGENNEFC 311	RA	RA
RESULT 12			RA	RA
Q8AAFI	PRELIMINARY;	PRT;	RA	RA
ID	Q8AAFI;	334 AA.	RA	RA
AC	Q8AAFI;	PRT;	RA	RA
DT	01-JUN-2003 (TREMBLrel. 24, Created)	DT	RA	RA
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	DT	RA	RA
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	RA	RA
DB	Hypothetical protein.	DB	RA	RA
GN	OrderredLocusName=BR0514;	GN	RA	RA
OS	Bacteroides thetaotaomicron.	OS	RA	RA
OC	Bacteroides; Bacteroidetes; Bacteroides (class); Bacteroidales;	OC	RA	RA
OC	Bacteroidaceae; Bacteroides.	OC	RA	RA
OX	NCBI_TaxID=818;	OX	RA	RA
RA	SEQUENCE FROM N.A.	RA	RA	RA
RA	STRAIN=VP482 / ATCC 29148;	RA	RA	RA
RA	MEDLINE=22550858; PubMed=12653928; DOI=10.1126/science.1080029;	RA	RA	RA
RA	Xu J., Bjurzell M.K., Hamrod J., Deng S., Carmichael L.K., Chiang H.C., Hooper L.V., Gordon J.I.;	RA	RA	RA
RA	"A genomic view of the human-Bacteroides thetaotaomicron symbiosis . . . ;	RA	RA	RA
RA	Science 299:204-2076 (2003).	RA	RA	RA
RA	DR: AE016928; AAO75621.1; -.	RA	RA	RA
RA	Complete proteome.	RA	RA	RA
RA	SEQUENCE 334 AA; MW: 39493 MW;	RA	RA	RA
RA	Query Match 46.9%; Score 46; DB 2; Length 334;	RA	RA	RA
RA	Best Local Similarity 66.7%; Pred. No. 40;	RA	RA	RA
RA	Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	RA	RA	RA
Qy	4 RGGFNNPRYC 15	4 RGGFNNPRYC 15	RA	RA
Db	71 RGSGFFNPRYC 82	71 RGSGFFNPRYC 82	RA	RA
RESULT 13			RA	RA
Q73LX3	PRELIMINARY;	PRT;	RA	RA
AC	Q73LX3;	354 AA.	RA	RA
AC	Q73LX3;	PRT;	RA	RA
DT	05-JUL-2004 (TREMBLrel. 27, Created)	DT	RA	RA
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT	RA	RA
DE	FemB family protein.	DE	RA	RA
Qy	1 CFFRGFFNNPRYC 15	1 CFFRGFFNNPRYC 15	RA	RA
Db	296 CYYGDSFFGENNEFC 310	296 CYYGDSFFGENNEFC 310	RA	RA
			RESULT 15	

Q9BUL0 PRELIMINARY; PRT; 393 AA.
 ID Q9BUL0; Q6P150;
 AC Q9BUL0; Q6P150;
 DT 01-JUN-2001 (TREMBurel, 17, Created)
 DT 01-JUN-2001 (TREMBurel, 17, Last sequence update)
 DT 25-OCT-2004 (TREMBurel, 28, Last annotation update)
 DE Suppressor of variegation 4-20 homolog 1, isoform 2.
 GN Name=SUVR40H1;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo
 NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta, and Testis;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strasberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Schulter G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Sharpen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bopak S.A., McEwan P.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whetley J., Heitton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whetley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Director MGC Project;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 CC Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 DR -1- SIMILARITY: Contains 1 SBT domain.
 DR EMBL; B002522; AAH02522.2;
 DR B0065287; AAH65287.1;
 DR InterPro; IPR001214; SET.
 DR Pfam; PF00856; SET; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS50280; SET; 1.
 SQ SEQUENCE 393 AA; 44618 MW; A9690C2164F384E CRC64;
 Query Match 46.9%; Score 46; DB 2; Length 393;
 Best Local Similarity 40.0%; Pred. No. 47;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CFPFGGFFNPRYC 15
 Db 305 CYYGDGFFGENNEFC 319

Search completed: October 4, 2005, 22:15:08
 Job time : 173 secs

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OM protein - protein search, using SW model

Run on: October 4, 2005, 22:03:45 ; Search time 42 Seconds (without alignments)

26,660 Million cell updates/sec

Title: US-10-633-423-2

Perfect score: 98

Sequence: 1 CFFRGFFNNPRYC 15

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74669064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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4: /cgn2_6_ptodata/1/iaa/5B_COMB.pep:*

5: /cgn2_6_ptodata/1/iaa/5CTUS_COMB.pep:*

6: /cgn2_6_ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	46	46.9	876	4	US-09-764-176-10	Sequence 10, Appl	Sequence 10, Appl
2	42	42.9	315	4	US-09-187-906-19	Sequence 19, Appl	Sequence 19, Appl
3	42	42.9	400	3	US-09-220-528-63	Sequence 63, Appl	Sequence 63, Appl
4	42	42.9	400	4	US-09-187-906-21	Sequence 21, Appl	Sequence 21, Appl
5	42	42.9	400	4	US-09-194-016-079	Sequence 90/9, Appl	Sequence 90/9, Appl
6	41	41.8	60	4	US-09-248-796A-2733/2	Sequence 2733/2, A	Sequence 2733/2, A
7	41	41.8	350	4	US-09-270-767-4355/7	Sequence 4355/7, A	Sequence 4355/7, A
8	41	41.8	521	2	US-08-504-048-9	Sequence 9, Appl	Sequence 9, Appl
9	41	41.8	653	4	US-09-171-937C-27	Sequence 27, Appl	Sequence 27, Appl
10	41	41.8	779	4	US-09-171-937C-25	Sequence 25, Appl	Sequence 25, Appl
11	40	40.8	495	4	US-09-489-039A-1052/8	Sequence 10/28, A	Sequence 10/28, A
12	40	40.8	588	4	US-09-252-991A-1857/8	Sequence 18/78, A	Sequence 18/78, A
13	40	40.8	713	2	US-08-849-212-4	Sequence 4, Appl	Sequence 4, Appl
14	40	40.8	832	2	US-09-489-039A-1243/8	Sequence 12/38, A	Sequence 12/38, A
15	39.5	40.3	313	3	US-08-990-379-7	Sequence 7, Appl	Sequence 7, Appl
16	39.5	40.3	314	3	US-09-164-193-22	Sequence 22, Appl	Sequence 22, Appl
17	39.5	40.3	314	4	US-09-221-448A-22	Sequence 22, Appl	Sequence 22, Appl
18	39.5	40.3	458	4	US-09-543-681A-6324	Sequence 6324, Appl	Sequence 6324, Appl
19	39	39.8	15	6	5227466-7	Patent No. 5227466	Patent No. 5227466
20	39	39.8	15	6	5227466-7	Patent No. 5227466	Patent No. 5227466
21	39	39.8	267	4	US-09-634-238-288	Sequence 288, Appl	Sequence 288, Appl
22	39	39.8	379	4	US-09-634-681A-7297	Sequence 7297, Appl	Sequence 7297, Appl
23	39	39.8	383	3	US-08-857-076-105	Sequence 105, Appl	Sequence 105, Appl
24	38.5	39.3	368	4	US-09-248-796A-1680/0	Sequence 1680/0, A	Sequence 1680/0, A
25	38.5	39.3	527	3	US-08-369-822C-25	Sequence 25, Appl	Sequence 25, Appl
26	38.5	39.3	527	3	US-08-582-776C-40	Sequence 40, Appl	Sequence 40, Appl
27	38.5	39.3	527	3	US-08-434-831B-37	Sequence 37, Appl	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-09-764-176-10

; Sequence 10, Application US/09764176

; Patent No. 6809189

; GENERAL INFORMATION:

; APPLICANT: NOTEBORN, Matthieu Hubertus Maria

; APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna Maria

; APPLICANT: ROHN, Jennifer Leigh

; APPLICANT: WEITS, Bertram

; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN

; FILE REFERENCE: 4725US

; CURRENT APPLICATION NUMBER: US/09/764,176

; CURRENT FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10

; LENGTH: 876

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Description of sequence: Amino acid sequence deduced from the nucleic acid sequence of APP-

US-09-764-176-10

; OTHER INFORMATION: leic acid sequence of APP-

Query Match 6;保守性 Matches 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CFFRGFFNNHNPYRC 15

Db 296 CYYGDDGFGENNEFC 310

RESULT 2

US-09-187-906-19

; Sequence 19, Application US/09187906

; Patent No. 6677135

; GENERAL INFORMATION:

; APPLICANT: BIOPRO, INC.

; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural

; NUMBER OF SEQ ID NOS: 21

; ADDRESS: Biogen, Inc.

; STREET: 14 Cambridge Center

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02142

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/187,906
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/07726
 FILING DATE: 07-MAY-97
 APPLICATION NUMBER: US 60/017,427
 FILING DATE: 08-MAY-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/019,300
 FILING DATE: 07-JUN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,859
 FILING DATE: 16-JUL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043,533
 FILING DATE: 10-APR-97
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaplan, Warren A.
 REGISTRATION NUMBER: 34,199
 REFERENCE/DOCKET NUMBER: A008 PCT CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-679-2400
 TELEFAX: 617-679-2838
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 315 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-187-906-19

Query Match Score 42; DB 4; Length 315;
 Best Local Similarity 58.3%; Pred. No. 66;
 Matches 7; Conservative 1; Nismatches 4; Indels 0; Gaps 0;

Qy 1 CFFRGFFFNHP 12
 Db 243 CEMLGFFSHNP 254

RESULT 3
 US-09-220-528-63
 Sequence 63, Application US/09220528A
 GENERAL INFORMATION:
 Patent No. 6284540
 APPLICANT: Milbrandt, Jeffrey D.
 TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
 FILE REFERENCE: 6029-7998
 CURRENT APPLICATION NUMBER: US/09/220,528A
 CURRENT FILING DATE: 1998-12-24
 EARLIER APPLICATION NUMBER: 09/218,698
 EARLIER FILING DATE: 1998-12-22
 EARLIER APPLICATION NUMBER: 60/108,148
 EARLIER FILING DATE: 1998-11-12
 EARLIER FILING DATE: 1998-09-29
 NUMBER OF SEQ ID NOS: 120
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 63
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-220-528-63

Query Match Score 42; DB 4; Length 400;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 1; Nismatches 4; Indels 0; Gaps 0;

Qy 1 CFFRGFFFNHP 12
 Db 328 CEMLGFFSHNP 339

Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 1; Nismatches 4; Indels 0; Gaps 0;

RESULT 4
 US-09-187-906-21
 Sequence 21, Application US/09187906
 Patient No. 6677135
 GENERAL INFORMATION:
 APPLICANT: BIOMAN, INC.
 TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Biogen, Inc.
 STREET: 14 Cambridge Center
 CITY: Cambridge
 STATE: MA
 ZIP: 02142
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/187,906
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/07726
 FILING DATE: 07-MAY-97
 APPLICATION NUMBER: US 60/017,427
 FILING DATE: 08-MAY-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/019,300
 FILING DATE: 07-JUN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,859
 FILING DATE: 16-JUL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043,533
 FILING DATE: 10-APR-97
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaplan, Warren A.
 REGISTRATION NUMBER: 34,199
 REFERENCE/DOCKET NUMBER: A008 PCT CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-679-2400
 TELEFAX: 617-679-2838
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 315 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-187-906-19

Query Match Score 42.9%; DB 4; Length 400;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 1; Nismatches 4; Indels 0; Gaps 0;

Qy 1 CFFRGFFFNHP 12
 Db 328 CEMLGFFSHNP 339

RESULT 5
 US-09-949-016-9079

Sequence 9079, Application US/09949016
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9079
 LENGTH: 400
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-9079

Query Match 42.9%; Score 42; DB 4; Length 400;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFFRGFFFNHNP 12
 Db 328 CEMLEGFFSHNP 339

RESULT 6
 US-09-248-796A-27332
 Sequence 27332, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 10/196,132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 27332
 LENGTH: 60
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-27332

Query Match 41.8%; Score 41; DB 4; Length 60;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGFFNHNPRYC 15
 Db 47 GGCFPFYPRYC 57

RESULT 7
 US-09-270-767-43557
 Sequence 43557, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17

Query Match 41.8%; Score 41; DB 2; Length 521;
 Best Local Similarity 46.7%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Query Match 41.8%; Score 41; DB 4; Length 350;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFRGGFFNIN 11
 Db 259 FYRGCFYFREN 268

RESULT 8
 US-08-504-048-9
 Sequence 9, Application US/08504048
 Patent No. 5843674
 GENERAL INFORMATION:
 APPLICANT: TAKIMOTO, Hiroyuki
 APPLICANT: SUZUKI, Satoshi
 APPLICANT: SHIBATA, Koushi
 APPLICANT: MASUI, Shigeaki
 TITLE OF INVENTION: ANTI-HUMAN TYROSINASE
 TITLE OF INVENTION: MONOCLONAL ANTIBODY
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/504,048
 FILING DATE:
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: SAT0127.001APC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-160-0404
 TELEX: 714-760-9502
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 521 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-504-048-9

Qy 1 CFFRGFFNHPRYC 15
 Db 99 CHCNGNFGNNGYC 113

RESULT 9
 US-09-171-937C-27
 / Sequence 27, Application US/09171937C
 / GENERAL INFORMATION:
 / APPLICANT: GODDIJN, Oscar Johannes Maria
 / PEn, Jan
 / SMEEKENS, Josephus Christianus M.
 / TITLE OF INVENTION: Regulating metabolism by modifying the
 / level of trehalose-6-phosphate
 / NUMBER OF SEQUENCES: 57
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: LADAS & PARRY
 / STREET: 26 WEST 61 STREET
 / CITY: NEW YORK
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10023
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-Dos/MS-Dos
 / SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/171,937C
 / FILING DATE: 28-Apr-1999
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: PCT/EP97/02497
 / FILING DATE: 02-MAY-1997
 / APPLICATION NUMBER: EP 96.201.225.8
 / FILING DATE: 03-MAY-1996
 / APPLICATION NUMBER: EP 96.202.128.3
 / FILING DATE: 26-JUL-1996
 / APPLICATION NUMBER: EP 96.202.395.8
 / FILING DATE: 29-AUG-1996
 / ATTORNEY/AGENT INFORMATION:
 / NAME: MASS, Clifford J.
 / REGISTRATION NUMBER: 30,086
 / REFERENCE/DOCKET NUMBER: U-011967-1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212) 708-1890
 / TELEFAX: (212) 246-8959
 / INFORMATION FOR SEQ ID NO: 25:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 779 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 / US-09-171-937C-25

Query Match 41.8%; Score 41; DB 4; Length 779;
 Best Local Similarity 58.3%; Pred. No. 2.4e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CFFRGFFNHP 12
 Db 130 CRFKIGFFLHSP 141

RESULT 11
 US-09-489-039A-10528
 / Sequence 10528, Application US/09489039A
 / Patent No. 6610816
 / GENERAL INFORMATION:
 / APPLICANT: Gary Breton et. al
 / TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 / TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 / FILE FILING DATE: 27/09/2004/001
 / CURRENT APPLICATION NUMBER: US/09/489,039A
 / CURRENT FILING DATE: 2006-01-27
 / PRIOR APPLICATION NUMBER: US 60/117,747
 / PRIOR FILING DATE: 1999-01-29
 / NUMBER OF SEQ ID NOS: 14342
 / SEQ ID NO. 10528
 / LENGTH: 495
 / TYPE: PRT
 / ORGANISM: Klebsiella pneumoniae
 / US-09-489-039A-10528

RESULT 10
 US-09-171-937C-25
 / Sequence 25, Application US/09171937C
 / Patent No. 6633490
 / GENERAL INFORMATION:
 / APPLICANT: GODDIJN, Oscar Johannes Maria
 / PEn, Jan

Query Match 40.8%; Score 40; DB 4; Length 495;
 Best Local Similarity 53.8%; Pred. No. 2.2e+02; Length 495;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CFFRGFFENHNPR 13
 Db 403 CFFTGFFVFGPQ 415

RESULT 12
 US-09-252-991A-18578
 ; Sequence 18578, Application US/09252991A
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196 136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-07-27
 ; ORGANISM: Pseudomonas aeruginosa
 ; SEQ ID NO: 18578
 ; LENGTH: 588

Query Match 40.8%; Score 40; DB 4; Length 588;
 Best Local Similarity 54.5%; Pred. No. 2.6e+02; Length 588;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 RGGEFFHNPRY 14
 Db 474 RGGFAGHGPKH 484

RESULT 13
 US-08-849-212-4
 ; Sequence 4, Application US/08849212
 ; Patent No. 5827698

GENERAL INFORMATION:
 APPLICANT: KIKUCHI, YOSHIMI
 APPLICANT: SUZUKI, TOMOKO
 APPLICANT: KOJIMA, HIROYUKI
 TITLE OF INVENTION: NOVEL LYSINE DECARBOXYLASE GENE AND
 TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
 NUMBER OF SEQUENCES: 6
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAYER & NEUSTADT,
 ADDRESS: P. C.
 STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/849,212
 FILING DATE: 9-TUN-1997
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 6/306386
 FILING DATE: 09-DEC-1994
 ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-7220
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 713 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-849-212-4

Query Match 40.8%; Score 40; DB 2; Length 713;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 FENHNPRYC 15
 Db 45 FIEHNPRC 53

RESULT 14
 US-09-489-039A-12438
 ; Sequence 12438, Application US/09489039A
 ; Patent No. 6610336

GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

Query Match 40.8%; Score 40; DB 4; Length 832;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 FENHNPRYC 15
 Db 160 FIEHNPRC 168

RESULT 15
 US-09-489-039A-12438
 ; Sequence 12438, Application US/09489039A
 ; Patent No. 6610336

GENERAL INFORMATION:
 APPLICANT: Stork, Phillip J.
 TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
 TITLE OF INVENTION: Their Biologically Active Expression Products

Query Match 40.8%; Score 40; DB 4; Length 832;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 FENHNPRYC 15
 Db 160 FIEHNPRC 168

RESULT 15
 US-08-99-379-7
 ; Sequence 7, Application US/08990379
 ; Patent No. 5998188

GENERAL INFORMATION:
 APPLICANT: Misra-Press, Anita
 TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
 TITLE OF INVENTION: Their Biologically Active Expression Products

Query Match 40.8%; Score 40; DB 4; Length 832;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 FENHNPRYC 15
 Db 160 FIEHNPRC 168

GENERAL INFORMATION:
 CURRENT FILING DATE: 1997-12-15
 EARLIER APPLICATION NUMBER: PCT/US96/10402
 EARLIER FILING DATE: 1996-06-14
 EARLIER APPLICATION NUMBER: 60/000,263
 EARLIER FILING DATE: 1995-06-16
 NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 7
 LENGTH: 313
 TYPE: PRT

ORGANISM: *Mus* sp.
US-08-990-379-7

Query Match 40.3%; Score 39.5; DB 2; Length 313;
Best Local Similarity 53.3%; Pred. No. 1. 6e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
Qy 1 CFFRGGFPNHNPRYC 15
| | | | | : | | | | |
Db 125 CFLRGFKSFQ-TYC 138

Search completed: October 4, 2005, 22:18:35
Job time : 43 secs

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES	
1	98	100.0	15	16	US-10-633-423-2	Sequence 2, Appli	Length: 15
2	98	100.0	15	16	US-10-633-423-2	Sequence 2, Appli	TYPE: PRT
3	53.5	54.6	453	15	US-10-369-493-6581	Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORGANISM: Artificial Sequence
4	53.5	54.6	453	15	US-10-369-493-6582		FEATURE: OTHER INFORMATION: Synthetic Sequence
5	53.5	54.6	453	15	US-10-369-493-6583		
6	50.5	51.5	267	16	US-10-425-115-191952	Sequence 191952, A	
7	50.5	51.5	293	15	US-10-425-114-36595	Sequence 36595, A	
8	50.5	51.5	366	16	US-10-425-115-191953	Sequence 191953,	
9	50	51.0	447	15	US-10-369-493-6450	Sequence 6450, Ap	
10	50	51.0	511	15	US-10-369-493-6353	Sequence 6353, Ap	
11	49	50.0	124	16	US-10-425-115-339901	Sequence 339901,	

```

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIORITY APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6582
LENGTH: 453
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-6582

Query Match      54.6%; Score 53.5; DB 15; Length 453;
Best Local Similarity 28.6%; Pred. No. 4.7; Gaps 2;
Matches 12; Conservative 3; Mismatches 0; Indels 27; Gaps 2;

Qy   1 CFPGGFFN-----HNP-----RYC 15
Db   160 CFTRGFFYNWEGGPSSNLFNLNPETPGHSPTDGNNSCTSAGRYC 201

RESULT 5
US-10-369-493-6583
Sequence 6583, Application US/10/369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIORITY APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6583
LENGTH: 453
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-6583

Query Match      54.6%; Score 53.5; DB 15; Length 453;
Best Local Similarity 28.6%; Pred. No. 4.7; Gaps 2;
Matches 12; Conservative 3; Mismatches 0; Indels 27; Gaps 2;

Qy   1 CFPGGFFN-----HNP-----RYC 15
Db   160 CFTRGFFYNWEGGPSSNLFNLNPETPGHSPTDGNNSCTSAGRYC 201

RESULT 6
US-10-445-115-191962
Sequence 191962, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yilinwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 363326

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SEQ ID NO 191962
 LENGTH: 267
 TYPE: PRT
 ORGANISM: *zea mays*
 OTHER INFORMATION: Clone ID: MRT4577_106656C.1.pep
 US-10-425-115-191962

Query Match 51.5%; Score 50.5%; DB 16; Length 267;
 Best Local Similarity 60.0%; Pred. No. 8.4;
 Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 CFFRGFFFNHNPRYC 15
 Db 73 CIFK-GLFNCSPRYC 86

RESULT 9
 US-10-369-493-6450
 ; Sequence 6450, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 8-10(5205)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6450
 ; LENGTH: 447;
 ; TYPE: PRT
 ; ORGANISM: *Caenorhabditis elegans*
 US-10-369-493-6450

Query Match 51.0%; Score 50.; DB 15; Length 447;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFRGFFFN 9
 Db 154 CFFRGFFYN 162

RESULT 10
 US-10-369-493-6353
 ; Sequence 6353, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 8-10(5205)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6353
 ; LENGTH: 511
 ; TYPE: PRT
 ; ORGANISM: *Caenorhabditis elegans*
 US-10-369-493-6353

Query Match 51.0%; Score 50.; DB 15; Length 511;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CFFRGFFFN 9
 Db 154 CFFRGFFYN 162

RESULT 8
 US-10-425-115-191953
 ; Sequence 191953, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; Title of Invention: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; LENGTH: 366
 ; TYPE: PRT
 ; ORGANISM: *zea mays*
 ; OTHER INFORMATION: Clone ID: MRT4577_106647C.1.pep
 US-10-425-115-191953

i NUMBER OF SEQ ID NOS: 74
i SOFTWARE: PatentIn ver. 2.0
i SEQ ID NO 42
i LENGTH: 166
i TYPE: PRT
i ORGANISM: Homo sapiens
i FEATURE:
i NAME/KEY: SITE
i LOCATION: (157)
i OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
us-09-764-861-42

Query Match 46.9%; Score 46; DB 9; Length 166;
Best Local Similarity 40.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CPPRGGFENPRYC 15
|:: ||| | :|
Db 114 CYYGDFERGENNEFC 128

Search completed: October 4, 2005, 22:31:06
Job time : 165 secs

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